# GenePattern

**FeatureSummaryViewer Documentation**

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| **Module name:** | FeatureSummaryViewer |
| **Description:** | Used to view a list of features from a predictor. |
| **Author:** | Ken Ross, Joshua Gould (Broad Institute) g-help@broad.mit.edu |
| **Date:** | 12/10/04 |
| **Release:** | 1.1 |

**Summary:** This is a tool that allows the user to view feature lists such as those produced by the KNN and weighted voting prediction algorithms (KNN, KNNXValidation,.WeightedVoting, and WeightedVotingXValidation). These tables have three columns: feature name, feature description, and number of times features used (for leave-one-out cross-validation). The viewer includes an interactive histogram of the features included in each cross validation run. Clicking on a point in the plot selects the corresponding element in the table and selecting an element in the table highlights the corresponding data point in the plot. Users can zoom in and out of the plot by clicking and dragging the mouse or by selecting View -> Zoom In or View -> Zoom Out. The scale of the plot can be reset to its original value by choosing the Reset menu item in the View menu. Elements in the table can be selected individually with the mouse. To select all table elements choose Edit -> Select All. Users can search for features by selecting Edit -> Find. Selected table elements can be copied by picking Edit -> Copy. Selecting File -> Save Image will save an image of the plot and selecting File -> Print will print the plot. To retrieve information about Affymetrix probe ids using GeneCruiser, choose the Select Annotations item under the GeneCruiser menu. Select the features you want to retrieve annotations for in the table. Next choose what fields to retrieve from GeneCruiser in the GeneCruiser dialog. Annotations will appear in additional columns in the table.

**References:**

- none

**Parameters:**

| Name | Description |
|---|---|
| feature_filename: | odf file with or without features to summarize |

**Return Value:** An R list with components:

1. Stdout: the "stdout" text output from running the program.
2. Stderr: the "stderr" error report from running the program.

**Platform dependencies:**

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| **Task type**: | Visualizer |
| **CPU type**: | any |
| **OS:** | any |
| **Java JVM level:** | 1.4 |
| **Language:** | Java |

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**Support files:**　　　　GeneCruiser.jar, GeneListSignificanceViewer.jar , axis.jar, commons-discovery.jar, commons-logging.jar, jai_codec.jar, jai_core.jar, jaxrpc.jar, plot.jar, saaj.jar, FeatureSummaryViewer.jar, qflib_12.jar, qfpp.jar, broad-cg.jar

**Native command line:**　　　　<java> -Dedu.mit.broad.gc.endpoint=http://www.broad.mit.edu/webservices/genecruiser/services/Annotation <java_flags> -cp <libdir>GeneCruiser.jar<path.separator><libdir>GeneListSignificanceViewer.jar<path.separator><libdir>axis.jar<path.separator><libdir>commons-discovery.jar<path.separator><libdir>commons-logging.jar<path.separator><libdir>jai_codec.jar<path.separator><libdir>jai_core.jar<path.separator><libdir>jaxrpc.jar<path.separator><libdir>plot.jar<path.separator><libdir>saaj.jar<path.separator><libdir>FeatureSummaryViewer.jar<path.separator><libdir>qflib_12.jar<path.separator><libdir>qfpp.jar<path.separator><libdir>broad-cg.jar edu.mit.broad.modules.features.FeatureViewFrame <feature.filename>